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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/060,369

DATE: 04/07/2003

TIME: 14:31:24

Input Set : A:\2931-104.txt

Output Set: N:\CRF4\04072003\J060369.raw

3 <110> APPLICANT: Zastawny, Roman
 5 <120> TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4
 7 <130> FILE REFERENCE: 2931-104
 9 <140> CURRENT APPLICATION NUMBER: US 10/060369
 C--> 10 <141> **CURRENT FILING DATE: 2003-03-31**
 12 <150> PRIOR APPLICATION NUMBER: US 09/173565
 13 <151> PRIOR FILING DATE: 1998-08-16
 15 <160> NUMBER OF SEQ ID NOS: 12
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 28
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: PCR primer
 27 <400> SEQUENCE: 1
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 34 <213> ORGANISM: Artificial Sequence
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 44 <211> LENGTH: 26
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
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 56 <211> LENGTH: 23
 57 <212> TYPE: DNA
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 63 <400> SEQUENCE: 4
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 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 50

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70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
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82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
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92 <211> LENGTH: 27
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
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97 <223> OTHER INFORMATION: PCR primer
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113 atgaatgaga aatgggacac aaactcttca gaaaactggc atcccatctg gaatgtcaat      180
115 gacacaaagc atcatctgta ctcatgatt aatattacct atgtgaacta ctatcttcac      240
117 cagcctcaag tggcagcaat cttcattatt tctactttc tgatcttctt tttgtgcatg      300
119 atgggaaata ctgtggtttg ctttattgta atgaggaaca aacatatgca cacagtcact      360
121 aatctcttca tcttaaacct ggccataagt gatttactag ttggcatatt ctgcatgcct      420
123 ataacactgc tggacaatat tatagcagga tggccatttg gaaacacgat gtgcaagatc      480
125 agtggattgg tccagggaat atctgtcgca gcttcagtct ttacgttagt tgcaattgct      540
127 gtagataggt tccagtgtgt ggtctacct tttaaaccaa agctcactat caagacagcg      600
129 tttgtcatta ttatgatcat ctgggtccta gccatcacca ttatgtctcc atctgcagta      660
131 atgttacatg tgcaagaaga aaaatattac cgagtgcgac tcaactccca gaataaaacc      720
133 agtccagtct actggtgccg ggaagactgg ccaaatcagg aaatgaggaa gatctacacc      780
135 actgtgctgt ttgccaacat ctacctggct cccctctccc tcattgtcat catgtatgga      840
137 aggattggaa tttcactctt cagggctgca gttcctcaca caggcaggaa gaaccaggag      900
139 cagtggcacg tgggtgtccag gaagaagcag aagatcatta agatgctcct gattgtggcc      960
141 ctgcttttta ttctctcatg gctgcccctg tggactctaa tgatgctctc agactacgct      1020
143 gacctttctc caaatgaact gcagatcatc aacatctaca tctacccttt tgcacactgg      1080
145 ctggcattcg gcaacagcag tgtcaatccc atcatttatg gtttcttcaa cgagaatttc      1140
147 cgccgtgggt tccaagaagc tttccagctc cagctctgcc aaaaaagagc aaagcctatg      1200
149 gaagcttata ccctaaaagc taaaagccat gtgctcataa acacatctaa tcagcttgct      1260
151 caggaatcta catttcaaaa ccctcatggg gaaaccttgc tttataggaa aagtgtgtaa      1320

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153 aaaccccaac aggaattagt gatggaagaa ttaaaagaaa ctactaacag cagtgaatt 1380
155 taaaaagagc tagtgtgata atcctaactc tactacgcat tatatattta aatccattgc 1440
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159 <211> LENGTH: 420
160 <212> TYPE: PRT
161 <213> ORGANISM: Human
163 <400> SEQUENCE: 9
165 Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp His Pro Ile
166 1 5 10 15
169 Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
170 20 25 30
173 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
174 35 40 45
177 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
178 50 55 60
181 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
182 65 70 75 80
185 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
186 85 90 95
189 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
190 100 105 110
193 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
194 115 120 125
197 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
198 130 135 140
201 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
202 145 150 155 160
205 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
206 165 170 175
209 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
210 180 185 190
213 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
214 195 200 205
217 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
218 210 215 220
221 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
222 225 230 235 240
225 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
226 245 250 255
229 Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile
230 260 265 270
233 Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
234 275 280 285
237 Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
238 290 295 300
241 Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
242 305 310 315 320
245 Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
246 325 330 335

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249 Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
250           340           345           350
253 Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu Lys Ala Lys
254           355           360           365
257 Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
258           370           375           380
261 Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
262 385           390           395           400
265 Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
266           405           410           415
269 Ser Ser Glu Ile
270           420
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 384
275 <212> TYPE: PRT
276 <213> ORGANISM: Human
278 <400> SEQUENCE: 10
280 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser
281 1           5           10           15
284 Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
285           20           25           30
288 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
289           35           40           45
292 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
293           50           55           60
296 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
297 65           70           75           80
300 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
301           85           90           95
304 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
305           100          105          110
308 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
309           115          120          125
312 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
313           130          135          140
316 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
317 145          150          155          160
320 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
321           165          170          175
324 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
325           180          185          190
328 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
329           195          200          205
332 Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
333           210          215          220
336 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
337 225          230          235          240
340 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
341           245          250          255

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344 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
345           260           265           270
348 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
349           275           280           285
352 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
353           290           295           300
356 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
357 305           310           315           320
360 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
361           325           330           335
364 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
365           340           345           350
368 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
369           355           360           365
372 Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
373           370           375           380
376 <210> SEQ ID NO: 11
377 <211> LENGTH: 444
378 <212> TYPE: PRT
379 <213> ORGANISM: Human
381 <400> SEQUENCE: 11
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384 1           5           10           15
387 Ser Ala Ser Glu Leu Asn Glu Thr Gln Glu Pro Phe Leu Asn Pro Thr
388           20           25           30
391 Asp Tyr Asp Asp Glu Glu Phe Leu Arg Tyr Leu Trp Arg Glu Tyr Leu
392           35           40           45
395 His Pro Lys Glu Tyr Glu Trp Val Leu Ile Ala Gly Tyr Ile Ile Val
396           50           55           60
399 Phe Val Val Ala Leu Ile Gly Asn Val Leu Val Cys Val Ala Val Trp
400 65           70           75           80
403 Lys Asn His His Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu
404           85           90           95
407 Ser Leu Ala Asp Val Leu Val Thr Ile Thr Cys Leu Pro Ala Thr Leu
408           100          105          110
411 Val Val Asp Ile Thr Glu Thr Trp Phe Phe Gly Gln Ser Leu Cys Lys
412           115          120          125
415 Val Ile Pro Tyr Leu Gln Thr Val Ser Val Ser Val Ser Val Leu Thr
416           130          135          140
419 Leu Ser Cys Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu
420 145          150          155          160
423 Met Phe Lys Ser Thr Ala Lys Arg Ala Arg Asn Ser Ile Val Ile Ile
424           165          170          175
427 Trp Ile Val Ser Cys Ile Ile Met Ile Pro Gln Ala Ile Val Met Glu
428           180          185          190
431 Cys Ser Thr Val Phe Pro Gly Leu Ala Asn Lys Thr Thr Leu Phe Thr
432           195          200          205
435 Val Cys Asp Glu Arg Trp Gly Gly Glu Ile Tyr Pro Lys Met Tyr His
436           210          215          220

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VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/060,369**

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